

SEQUENCE LISTING

<110> Whitehead Institute for Biomedical Research
Hug, Christopher
Lodish, Harvey F.

<120> USE OF T-CADHERIN AS A TARGET

<130> SER-100X

<150> US 60/526,956

<151> 2003-12-03

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 713

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1) .. (22)

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<221> LIPID

<222> (693) .. (693)

<223> GPI-ANCHOR

<220>

<221> PROPEP

<222> (23) .. (139)

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<221> PROPEP

<222> (694) .. (713)

<223>

<400> 1

Met Gln Pro Arg Thr Pro Leu Val Leu Cys Val Leu Leu Ser Gln Val
1 5 10 15

Leu Leu Leu Thr Ser Ala Glu Asp Leu Asp Cys Thr Pro Gly Phe Gln
20 25 30

Gln Lys Val Phe His Ile Asn Gln Pro Ala Glu Phe Ile Glu Asp Gln
35 40 45

Ser Ile Leu Asn Leu Thr Phe Ser Asp Cys Lys Gly Asn Asp Lys Leu
50 55 60

Arg Tyr Glu Val Ser Ser Pro Tyr Phe Lys Val Asn Ser Asp Gly Gly

65		70		75		80
Leu Val Ala	Leu Arg Asn Ile Thr Ala Val Gly Lys Thr Leu Phe Val					
	85			90		95
His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val						
	100		105			110
Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala						
	115		120			125
Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro						
	130		135		140	
Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly						
	145		150		155	160
Lys Val Val Asp Ser Asp Arg Pro Glu Arg Ser Lys Phe Arg Leu Thr						
	165		170			175
Gly Lys Gly Val Asp Gln Glu Pro Lys Gly Ile Phe Arg Ile Asn Glu						
	180		185			190
Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Val Ile						
	195		200		205	
Ala Val Tyr Gln Leu Phe Val Glu Thr Thr Asp Val Asn Gly Lys Thr						
	210		215		220	
Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp						
	225		230		235	240
Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu						
	245		250			255
Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala						
	260		265			270
Asp Asp Pro Ala Thr Asp Asn Ala Leu Leu Arg Tyr Asn Ile Arg Gln						
	275		280		285	
Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu						
	290		295		300	
Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu						
	305		310		315	320
Thr Leu Glu Asn Pro Lys Tyr Glu Leu Ile Ile Glu Ala Gln Asp Met						
	325		330			335
Ala Gly Leu Asp Val Gly Leu Thr Gly Thr Ala Thr Ala Thr Ile Met						
	340		345			350
Ile Asp Asp Lys Asn Asp His Ser Pro Lys Phe Thr Lys Lys Glu Phe						
	355		360		365	
Gln Ala Thr Val Glu Glu Gly Ala Val Gly Val Ile Val Asn Leu Thr						
	370		375		380	

Val Glu Asp Lys Asp Asp Pro Thr Thr Gly Ala Trp Arg Ala Ala Tyr
 385 390 395 400
 Thr Ile Ile Asn Gly Asn Pro Gly Gln Ser Phe Glu Ile His Thr Asn
 405 410 415
 Pro Gln Thr Asn Glu Gly Met Leu Ser Val Val Lys Pro Leu Asp Tyr
 420 425 430
 Glu Ile Ser Ala Phe His Thr Leu Leu Ile Lys Val Glu Asn Glu Asp
 435 440 445
 Pro Leu Val Pro Asp Val Ser Tyr Gly Pro Ser Ser Thr Ala Thr Val
 450 455 460
 His Ile Thr Val Leu Asp Val Asn Glu Gly Pro Val Phe Tyr Pro Asp
 465 470 475 480
 Pro Met Met Val Thr Arg Gln Glu Asp Leu Ser Val Gly Ser Val Leu
 485 490 495
 Leu Thr Val Asn Ala Thr Asp Pro Asp Ser Leu Gln His Gln Thr Ile
 500 505 510
 Arg Tyr Ser Val Tyr Lys Asp Pro Ala Gly Trp Leu Asn Ile Asn Pro
 515 520 525
 Ile Asn Gly Thr Val Asp Thr Thr Ala Val Leu Asp Arg Glu Ser Pro
 530 535 540
 Phe Val Asp Asn Ser Val Tyr Thr Ala Leu Phe Leu Ala Ile Asp Ser
 545 550 555 560
 Gly Asn Pro Pro Ala Thr Gly Thr Gly Thr Leu Leu Ile Thr Leu Glu
 565 570 575
 Asp Val Asn Asp Asn Ala Pro Phe Ile Tyr Pro Thr Val Ala Glu Val
 580 585 590
 Cys Asp Asp Ala Lys Asn Leu Ser Val Val Ile Leu Gly Ala Ser Asp
 595 600 605
 Lys Asp Leu His Pro Asn Thr Asp Pro Phe Lys Phe Glu Ile His Lys
 610 615 620
 Gln Ala Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr
 625 630 635 640
 His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn
 645 650 655
 Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile
 660 665 670
 Thr Asp Leu Arg Val Gln Val Cys Ser Cys Arg Asn Ser Lys Val Asp
 675 680 685

Cys Asn Ala Ala Gly Ala Leu Arg Phe Ser Leu Pro Ser Val Leu Leu
 690 695 700

Leu Ser Leu Phe Ser Leu Ala Cys Leu
 705 710

<210> 2
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(14)
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 <222> (42)..(107)
 <223> Collagen-like domain

<220>
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 <222> (108)..(244)
 <223> Clq domain

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Met Leu Leu Leu Gly Ala Val Leu Leu Leu Leu Ala Leu Pro Gly His
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Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro
 20 25 30

Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly
 35 40 45

His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu
 50 55 60

Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile
 65 70 75 80

Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly
 85 90 95

Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg
 100 105 110

Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met
 115 120 125

Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp
 130 135 140

Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe

145 150 155 160
 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe
 165 170 175
 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn
 180 185 190
 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly
 195 200 205
 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu
 210 215 220
 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr
 225 230 235 240

His Asp Thr Asn

<210> 3
 <211> 247
 <212> PRT
 <213> Mus musculus

<220>
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 <222> (1)..(17)
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<220>
 <221> DOMAIN
 <222> (45)..(110)
 <223> Collagen-like domain

<220>
 <221> DOMAIN
 <222> (111)..(247)
 <223> Clq domain

<400> 3

Met Leu Leu Leu Gln Ala Leu Leu Phe Leu Leu Ile Leu Pro Ser His
 1 5 10 15
 Ala Glu Asp Asp Val Thr Thr Thr Glu Glu Leu Ala Pro Ala Leu Val
 20 25 30
 Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly
 35 40 45
 His Pro Gly His Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr
 50 55 60
 Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys
 65 70 75 80
 Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly
 85 90 95

Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr
 100 105 110
 Met Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val
 115 120 125
 Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn
 130 135 140
 His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu
 145 150 155 160
 Tyr Tyr Phe Ser Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val
 165 170 175
 Ser Leu Phe Lys Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr
 180 185 190
 Gln Glu Lys Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu
 195 200 205
 Glu Val Gly Asp Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His
 210 215 220
 Asn Gly Leu Tyr Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe
 225 230 235 240
 Leu Leu Tyr His Asp Thr Asn
 245

<210> 4
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 <212> PRT
 <213> Mus musculus

<220>
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 <223> GPI-ANCHOR

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 <222> (694)..(714)
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<400> 4

Met Gln Pro Arg Thr Pro Leu Thr Leu Cys Val Leu Leu Ser Gln Val
 1 5 10 15
 Leu Leu Val Thr Ser Ala Asp Asp Leu Glu Cys Thr Pro Gly Phe Gln
 20 25 30
 Arg Lys Val Leu His Ile His Gln Pro Ala Glu Phe Ile Glu Asp Gln
 35 40 45
 Pro Val Leu Asn Leu Thr Phe Asn Asp Cys Lys Gly Asn Glu Lys Leu
 50 55 60
 His Tyr Glu Val Ser Ser Pro His Phe Lys Val Asn Ser Asp Gly Thr
 65 70 75 80
 Leu Val Ala Leu Arg Asn Ile Thr Ala Val Gly Arg Thr Leu Phe Val
 85 90 95
 His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val
 100 105 110
 Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala
 115 120 125
 Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro
 130 135 140
 Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly
 145 150 155 160
 Lys Val Val Asp Ser Asp Arg Pro Glu Gly Ser Lys Phe Arg Leu Thr
 165 170 175
 Gly Lys Gly Val Asp Gln Asp Pro Lys Gly Thr Phe Arg Ile Asn Glu
 180 185 190
 Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Thr Ile
 195 200 205
 Ala Thr Tyr Gln Leu Tyr Val Glu Thr Thr Asp Ala Ser Gly Lys Thr
 210 215 220
 Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp
 225 230 235 240
 Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu
 245 250 255
 Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala
 260 265 270
 Asp Asp Pro Ala Thr Asp Asn Ala Leu Trp Arg Tyr Asn Ile Arg Gln
 275 280 285
 Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu
 290 295 300
 Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu

305		310		315		320									
Thr	Leu	Glu	Asn	Pro	Lys	Tyr	Glu	Leu	Ile	Ile	Glu	Ala	Gln	Asp	Met
			325						330					335	
Ala	Gly	Leu	Asp	Val	Gly	Leu	Thr	Gly	Thr	Ala	Thr	Ala	Thr	Ile	Val
			340					345					350		
Ile	Asp	Asp	Lys	Asn	Asp	His	Ser	Pro	Lys	Phe	Thr	Lys	Lys	Glu	Phe
		355					360					365			
Gln	Ala	Arg	Val	Glu	Glu	Gly	Ala	Val	Gly	Val	Ile	Val	Asn	Leu	Thr
	370					375					380				
Val	Glu	Asp	Lys	Asp	Asp	Pro	Thr	Thr	Gly	Ala	Trp	Arg	Ala	Ala	Tyr
385					390					395					400
Thr	Ile	Ile	Asn	Gly	Asn	Pro	Gly	Gln	Ser	Phe	Glu	Ile	His	Thr	Asn
			405					410						415	
Pro	Gln	Thr	Asn	Glu	Gly	Met	Leu	Ser	Val	Val	Lys	Pro	Leu	Asp	Tyr
			420				425						430		
Glu	Ile	Ser	Ala	Phe	His	Thr	Leu	Leu	Ile	Lys	Val	Glu	Asn	Glu	Asp
		435					440					445			
Pro	Leu	Val	Pro	Asp	Val	Ser	Tyr	Gly	Pro	Ser	Ser	Thr	Ala	Thr	Val
	450					455					460				
His	Ile	Thr	Val	Leu	Asp	Val	Asn	Glu	Gly	Pro	Val	Phe	Tyr	Pro	Asp
465					470					475					480
Pro	Met	Met	Val	Thr	Lys	Gln	Glu	Asn	Ile	Ser	Val	Gly	Ser	Val	Leu
				485					490					495	
Leu	Thr	Val	Asn	Ala	Thr	Asp	Pro	Asp	Ser	Leu	Gln	His	Gln	Thr	Ile
			500					505					510		
Arg	Tyr	Ser	Ile	Tyr	Lys	Asp	Pro	Ala	Gly	Trp	Leu	Ser	Ile	Asn	Pro
		515					520					525			
Ile	Asn	Gly	Thr	Val	Asp	Thr	Thr	Ala	Val	Leu	Asp	Arg	Glu	Ser	Pro
	530					535					540				
Phe	Val	His	Asn	Ser	Val	Tyr	Thr	Ala	Leu	Phe	Leu	Ala	Ile	Asp	Ser
545					550					555					560
Gly	Asn	Pro	Pro	Ala	Thr	Gly	Thr	Gly	Thr	Leu	Leu	Ile	Thr	Leu	Glu
				565					570					575	
Asp	Ile	Asn	Asp	Asn	Ala	Pro	Val	Ile	Tyr	Pro	Thr	Val	Ala	Glu	Val
			580					585					590		
Cys	Asp	Asp	Ala	Arg	Asn	Leu	Ser	Val	Val	Ile	Leu	Gly	Ala	Ser	Asp
		595					600					605			
Lys	Asp	Leu	His	Pro	Asn	Thr	Asp	Pro	Phe	Lys	Phe	Glu	Ile	His	Lys
	610					615					620				

Gln Thr Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr
 625 630 635 640

His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn
 645 650 655

Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile
 660 665 670

Thr Asp Leu Lys Val Gln Val Cys Ser Cys Lys Asn Ser Lys Val Asp
 675 680 685

Cys Asn Gly Ala Gly Ala Leu His Leu Ser Leu Ser Leu Leu Leu Leu
 690 695 700

Phe Ser Leu Leu Ser Leu Leu Ser Gly Leu
 705 710

<210> 5
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 <213> Artificial

<220>
 <223> primer

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 aagaattccg ccaccatgct actgttgcaa gctctc

36

<210> 6
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 6
 gactacaagg acgacgatga caaggaagat gacgttacta caact

45

<210> 7
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 7
 cttgtcatcg tcgtccttgt agtcggcatg actgggcagg attaa

45

<210> 8
 <211> 30
 <212> DNA

<213> Artificial

<220>

<223> primer

<400> 8

tttgaattct cagttggtat catggtagag

30

<210> 9

<211> 36

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 9

aagaattccg ccaccatgct actggtgcaa gctctc

36

<210> 10

<211> 60

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 10

tttgaattct cacttgctgt catcgtcttt gtagtctgca cttgcatcgt tggatatcatg

60

<210> 11

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 11

gacatctcct gtcccaag

18

<210> 12

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 12

ctaacatggt ctacatcg

18

<210> 13

<211> 18

<212> DNA
<213> Artificial

<220>
<223> primer

<400> 13
ctgtccacat cacagtcc

18

<210> 14
<211> 19
<212> DNA
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<400> 14
cagacagtcc ctgataaag

19

<210> 15
<211> 20
<212> DNA
<213> Artificial

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<400> 15
ctcgttgccc ttgcagtcac

20

<210> 16
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<223> primer

<400> 16
gacttccaga ggcactggc

19

<210> 17
<211> 19
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 17
ggctcctgtg gtgggggtcg

19

<210> 18

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ggttgccact gtcgatgg